NCBI

Single Nucleotide Polymorphism

dbSNP BUILD 110

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Reference SNP Cluster Report

NCBI SNP CLUSTER ID:	**rs5962**
Organism:	human (*Homo sapiens*)
Variation Class:	SNP: single nucleotide polym
Molecule Type:	Genomic
dbSNP build of first appearance:	52 9/99
dbSNP build of most recent change to cluster:	52
Current dbSNP build:	110

SNP Details are categorized in the following sections:

Submission | Fasta | Resource | Locus | Map | Varia

Submitter records for this RefSNP Cluster

The submission **ss7572** has the longest flanking sequence of all cluster members BLAST analysis for the current build.

NCBI Assay ID	Handle|Submitter ID	Validation Status	Entry Date	Update Date	Build Adde
ss7572	WIAF-CSNP|WIAF-11044	✓	07/15/99	01/29/01	52

Fasta sequence (Legend)

>gnl|dbSNP|rs5962|allelePos=101|totalLen=201|taxid=9606|snpclass=1|alleles='

TGGCACCCTT GGGCCAGCCC AGCCTCCATT TCTCCAGCTG TCCCCAGAGC CAACGTGC
CTCCTTTGGC AGTCACACGG AAGCTCTGCA GCCTGGACAA
Y
GGGGACTGTG ACCAGTTCTG CCACGAGGAA CAGAACTCTG TGGTGTGCTC CTGCGCCC

[redacted] GGGTACACCC TGGCTGACAA CGGCAAGGCC TGCATTCCCA

NCBI Resource Links

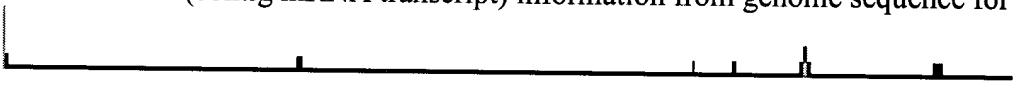
Submitter-Referenced Accessions:
GenBank: L00394

dbSNP Blast Analysis:
GenBank HTGS Finished: AB005892.1 AF503510.1 AL137002.1

LocusLink Analysis

LocusLink via analysis of contig annotation: F10 coagulation factor X

Gene Model (contig mRNA transcript) information from genome sequence for



Contig accession	Contig position	Protein accession	Function	dbSNP allele	Protein residue	Cod posi
NT_027140	1291267	NP_000495	contig reference	C	Asn [N]	3
			synonymous change	T	Asn [N]	3

LocusLink via BLAST analysis of mRNAs: F10 coagulation factor X
Variations are assigned to a gene if mapped within 2 kb of mRNA sequence feature.

Accession class	Nucleotide accession	Nucleotide Position	Hit orientation	Protein accession	Function
HTGS finished	AB005892.1	105	plus strand	BAA21634.1	locus

Integrated Maps:

NCBI MapViewer: rs5962 maps exactly once on NCBI human chromosome 1:

Chromosome	Contig accession	Contig Position	Chromosome Position	Hit orientation
13	NT_027140.5	1291267	108432435	plus strand

NCBI Sequence Viewer: See rs5962 in Sequence Viewer.

Project Ensembl: Query rs5962 in Ensembl.

UC Santa Cruz Genome Assembly: Query rs5962 on the Santa Cruz Assembly

Variation Summary:

Assay sample size (number of chromosomes):	114
Population data sample size (number of chromosomes):	106
Total number of populations with frequency data:	1
Total number of individuals with genotype data:	0
Average estimated heterozygosity:	0.047
Average Allele Frequency:	
C	0.972
T	0.028

Validation Summary:

Marker displays Mendelian segregation:	UNKNOWN
PCR results confirmed in multiple reactions:	YES
Homozygotes detected in individual genotype data:	UNKNOWN
Validation status:	

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